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FIGURE 1

1	AGCTCCAGCCTAGGCGTTCTACCTGGAAGAATGCAGGGGCCAGTACCTAGGACTGAGGA	60
61	AGATGGCTGACATCCAGAAACATTTTCGCTGGACAGCCAGGAGCGTAGGGCTGTGGCAG	120
121	TGCCCTGTGATCTTTGCCCTCATCTTCTGTTGGCATGTTGGCAATGGGCTGGTGTGG	180
181	CTGTGCTACTGCAGCCTGGCCCAAGTGCCCTGGCAGGAGCCAAAGCAGTACCACAGATCTCT	240
241	TCATCCTCAACTTGGCCGTGGCCGACCTTTTGCCTTCATCTGCTGCTGCCCTTCCAGG	300
301	CAGCCATCTACACACTGGATGCCCTGGCTCTTTGGGCTTTTCGTGTCAAGACGGTACATC	360
361	TGCTCATCTACCTACCATGTATGCCAGCAGCTTCACTGGCGGCCGTCTCCCTGGACA	420
421	GGTACCTGGCTGTGGGCACCCACTGCCCTCCAGAGCCCTGCCACCCCGCAACGCCG	480
481	GCGCCGCCGTGGGCTCGTGTGGCTGTGGCGGCTCTTTTCCGCGCCCTACCTAAGCT	540
541	ATTACGGCACGGTGGCTACGGCGGCTCGAGCTCTGCGTGCCCGCTTGGAGGACGCGC	600
601	GGCGCGCGGCTGGACGTGGCCACCTTCGCCCGGGCTACCTGCTGCCGTTGGCGCTGG	660
661	TGAGCCTGGCCTACGGACGACGCTATGTTTCTATGGGCCCGCGTGGGTCCCGCGGCG	720
721	CGCGGCGCAGCAGAGCGCGCAGAGCGGCGACCGCGCGGGGACGCGCCATGCTGGCAG	780
781	TGGCCGCGCTCTACGCGCTTTGCTGGGCGCCGACCCAGCGCTCATCTCTGCTTCTGGT	840
841	ACGGCCGCTTCGCCCTTCAGCCCGGCCACCTACGCTGTGCGCTGGCTCGCACTGCCCTCG	900
901	CCTACGCCCAACTCCTGCCCTTAACCGCTCGTCTACTCGCTCGCTCGCGCCACTTCCGCG	960
961	CGCGCTTCGCGCGCTGTGGCCCTGCGGCGCTCGCGCCACCGCCACCCACCGCGCTC	1020
1021	ATCGAGCCCTCCGTCGTGTCCAGCCGGCGCTTCGGGCCCGCGGTTATCCCGCGGACG	1080
1081	CCAGGCCCTCGTGTGGAGTATGGAGCCAGAGGGGATGCTCTGCGTGGTGGAGAGA	1140
1141	CTAGACTAACCTGTCCCCCAGGGACCTCAATAAACCCTGCCCGCTTGGACTCTGACGTC	1200
1201	TGTCAGAAATGCCACCAAGGAACATCTAGGGAACGGCAGTCTCGCCAGGCTCCACCAAAA	1260
1261	GCAGAAGCAAAGTTGCAGGG	1280

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20 40 60 80 100 120 140 160 180 200 220 240 260 280 300 320 340 360 370

V A F A L R R Y R V A V Y A A H A T
A L L Q H D A S A V G A W L R A D E
V V D F V L N L D A A L F C F R G G
A L T P T S R Y E V P M C H H H P G
G G T V K V P P W P G A L S R H Y G
V N S C C A T A A L V R I A S H G R
S G S C V A R S P L A G L L A R A L
G V P L F L L F V Y A A A R L H P A
P M E I A T A L C G W R H C S R G D
S G Q F G F R A L A L G H A Y R S G
D L W C F S S A E A F T P Y V R S R Q
L L A L L S R L L F C A G T L G A P P
S F S D W A L L A T L R W A P C P E G
I I P A A Y P W G A T R C P N P Q M R
N L G V D M H V Y V R R L S L W V S P
Q A P A L T R L R D G A A F C L R W S
I F Q L T L V G V L Y E Y A S R R G L
D I L N Y Y A V T A A A L F N R L R T
A V L L I I L A G R L A A R A F A P L
M P V I A L Y A Y R S A A G Y R R R R

1 21 41 61 81 101 121 141 161 181 201 221 241 261 281 301 312 341 361

FIGURE 2

202F40" CHE9000T

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FIGURE 3

1	CACTCAGCGATGACTTTGGCTCTGCTCTCCCTCCTCCATCTCCACGAGCTTCCAGCCC	60
61	AGAACAACCTGGCCAGACCCAGGTCGGGGAGTTAGATCCCGGGTCAAGCAACAGAACT	120
121	GGGGGCTCTTGCCCTGAGGATTCCAGCTTCTTCCAGGTGCCCTCTGATGGGAGATG	180
181	GCTGATGCCCAGAACATTTCACTGGACAGCCAGGAGTGTGGGGCCGTGGCAGTGCCCT	240
241	GTGGTCTTTGCCCCAATCTTCCCTGGGCACAGTGGGCAATGGGCTGGTGTGGCAGTG	300
301	CTCCTGCAGCCTGGCCGAGTGCCCTGGCAGGAGCCTGGCAGCACACGACCTGTTTCATC	360
361	CTCAACCTGGCGGTGGCTGACCTCTGCTTCACTTCACTGCTGCTGCCCTTCCAGGCCACC	420
421	ATCTACACGCTGGATGCCCTGGCTCTTTGGGGCCCTCGTCTGCAAGGCCGTGCACCTGCTC	480
481	ATCTACCTCACCATGTACGCCAGCAGCTTTACGCTGGCTGCTTCCGTGGACAGGTAC	540
541	CTGGCCGTGGGCACCCGCTGCGCTCGCGCCCTGGGCACGCCGCCGTAAACGCCCGGCC	600
601	GCAGTGGGCTGGTGTGGCTGCTGGCGGGCTCTTCTCGGGCCCTACCTCAGCTACTAC	660
661	GGACCCGTGCGCTACGGCGCGCTGGAGCTCTGCGTGGCCCGCTGGGAGGACCGCGCCGC	720
721	CGCGCCCTGGACGTGGCCACCTTCGCTGCCGGCTACCTGCTGCCCGTGGCTGTGGTGAGC	780
781	CTGGCCCTACGGCGCACGCTGCGCTTCCTGTGGCCCGCTGGGTCCCGCGGCGCGCG	840
841	GCGGCCGAGCGCGCGGAGGCGCACGGCCCGCGCGCGCGCATGCTGGCGGTGGCC	900
901	GCGCTCTACCGGCTCTGCTGGGTCGCGCACACGCGCTCATCCTGTGCTTCTGGTACGGC	960
961	CGCTTCGCCCTTCAGCCCGGCCACCTACGCCCTGCCGCCCTGGCCCTCACACTGCCCTGGCCCTAC	1020
021	GCCAACTCCTGCCCTCAACCCGCTCGTCTACGCGCTCGCCCTCGGCCACTTCCGCGCGCGC	1080
081	TTCCGCCCGCTGTGGCCGTGGCCCGCCGACGCCGCCACCGTGCCTCCCGCCCTTGGCT	1140
141	CGCGTCCGCCCGCGTCTCGGGCCCAACCCGGCTGCCCGGAGACGCCCGCCCTAGCGGG	1200
201	AGGCTGCTGGCTGGTGGCGGCCAGGGCCCGGAGCCCAAGGAGGACCCGTCCACGGCGGA	1260
261	GAGGCTGCCCGAGGACCGGAATAAACCCTGCCCGCTGGACTCCGCCCTGTGTCCGCTGTGTC	1320
321	TCACTCCCGTTCTCCGAAGCGGGAGCGCCACCGGGCCAGGATGGGCAATGCCACGAGC	1380
381	TCCTCTAGGGGCGTTGAGTGGAGCGACTTGTCCCCGC	1417

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FIGURE 4

1	H	S	A	M	T	L	A	L	V	L	L	G	A	L	L	G	S	P	P	S	P	T	S	F	Q	P	20
21	R	T	P	G	Q	T	Q	Q	V	L	I	A	I	P	V	A	G	R	G	R	G	T	A	R	R	T	40
41	G	G	S	C	L	R	I	I	N	L	I	S	F	S	L	D	S	I	P	C	P	S	D	G	E	M	60
61	A	D	A	Q	A	I	I	P	V	L	I	S	F	S	L	D	S	I	P	C	P	V	A	V	P	P	80
81	V	V	F	A	P	A	P	A	L	L	L	L	L	L	L	L	L	L	L	L	L	V	A	V	P	100	
101	L	L	Q	A	P	A	P	A	L	L	L	L	L	L	L	L	L	L	L	L	L	V	A	V	P	120	
121	L	N	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	V	A	V	P	140	
141	I	Y	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	V	A	V	P	160	
161	I	Y	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	V	A	V	P	180	
181	L	A	V	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	V	A	V	P	200	
201	A	V	G	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	V	A	V	P	220	
221	G	T	V	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	V	A	V	P	240	
241	R	A	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	V	A	V	P	260	
261	L	A	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	V	A	V	P	280	
281	A	A	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	V	A	V	P	300	
301	A	A	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	V	A	V	P	320	
321	R	A	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	V	A	V	P	340	
341	A	A	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	V	A	V	P	360	
361	F	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	V	A	V	P	380	
381	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	V	A	V	P	400	
401	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	V	A	V	P	420	
421	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	V	A	V	P	440	

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FIGURE 5A

hGALR3	M A D A Q N I S L D S P G	13
rGALR3	M A D I Q N I S L D S P G	13
rGALR1	M E L A P V N L S E G N G S D P E P P A E P R P L		25
		I	
hGALR3	. . . S V G A V A V P V V F A L I F L L G T V G N		35
rGALR3	. . . S V G A V A V P V V I F A L I F L L G M V G N		35
rGALR1	F G I G V E N F I T L V V F F G L I F A M G V L G N		50
		I	
hGALR3	G L V L A V L L Q P G P S A W Q E P G S T T D L F		60
rGALR3	G L V L A V L L Q P G P S A W Q E P S S T T D L F		60
rGALR1	S L V I T V L A R S K P G . . . K P R S T T N L F		72
	II		
hGALR3	I L N L A V A D L C F I L C C V P F Q A T I Y T L		85
rGALR3	I L N L A V A D L C F I L C C V P F Q A A I Y T L		85
rGALR1	I L N L S I A D L A Y L L F C I P F Q A T V Y A L		97

	III																									
hGALR3	D	A	W	L	F	G	A	L	V	C	K	A	V	H	L	L	I	Y	L	T	M	Y	A	S	S	110
rGALR3	D	A	W	L	F	G	A	F	V	C	K	T	V	H	L	L	I	Y	L	T	M	Y	A	S	S	110
rGALR1	P	T	W	V	L	G	A	F	I	C	K	F	I	H	Y	F	F	T	V	S	M	L	V	S	I	122
hGALR3	F	T	L	A	A	V	S	V	D	R	Y	L	A	V	R	H	P	L	R	S	R	A	L	R	T	135
rGALR3	F	T	L	A	A	V	S	L	D	R	Y	L	A	V	R	H	P	L	R	S	R	A	L	R	T	135
rGALR1	F	T	L	A	A	M	S	V	D	R	Y	V	A	I	V	H	S	R	S	S	S	L	R	V	147	
hGALR3	P	R	N	A	R	A	A	V	G	L	V	W	L	L	A	A	L	F	S	A	P	Y	L	S	Y	160
rGALR3	P	R	N	A	R	A	A	V	G	L	V	W	L	L	A	A	L	F	S	A	P	Y	L	S	Y	160
rGALR1	S	R	N	A	L	L	G	V	G	F	I	W	A	L	S	I	A	M	A	S	P	.	V	A	Y	171
hGALR3	Y	G	T	V	.	.	R	Y	G	A	L	E	L	C	V	P	A	W	.	E	D	A	R	R	R	182
rGALR3	Y	G	T	V	.	.	R	Y	G	A	L	E	L	C	V	P	A	W	.	E	D	A	R	R	R	182
rGALR1	Y	Q	R	L	F	H	R	D	S	N	Q	T	F	C	W	E	H	W	P	N	Q	L	H	K	K	196

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FIGURE 5C

hGALR3	A	L	D	V	A	T	F	A	A	G	Y	L	L	P	V	A	V	V	S	L	A	Y	G	R	T	207	
rGALR3	A	L	D	V	A	T	F	A	A	G	Y	L	L	P	V	A	V	V	S	L	A	Y	G	R	T	207	
rGALR1	A	Y	V	V	C	T	F	V	F	G	Y	L	L	P	L	L	I	C	F	C	Y	A	K	V	221		
V																											
hGALR3	L	R	F	L	W	A	A	V	G	P	A	G	A	A	A	E	A	R	R	R	A	T	G	R	232		
rGALR3	L	C	F	L	W	A	A	V	G	P	A	G	A	A	A	E	A	R	R	R	A	T	G	R	232		
rGALR1	L	N	H	L	H	K	K	L	K	N	M	S	K	K	S	E	A	S	K	K	242		
VI																											
hGALR3	A	G	R	A	M	L	A	V	A	A	L	Y	A	L	C	W	G	P	H	H	A	L	I	L	C	257	
rGALR3	A	G	R	A	M	L	A	V	A	A	L	Y	A	L	C	W	G	P	H	H	A	L	I	L	C	257	
rGALR1	T	A	Q	T	V	L	V	V	V	V	V	F	G	I	S	W	L	P	H	H	V	I	H	L	W	267	
VII																											
hGALR3	F	W	Y	G	R	F	A	F	S	P	A	T	Y	A	C	R	L	A	S	H	C	L	A	Y	A	282	
rGALR3	F	W	Y	G	R	F	A	F	S	P	A	T	Y	A	C	R	L	A	S	H	C	L	A	Y	A	282	
rGALR1	A	E	F	G	A	F	P	L	T	P	A	S	F	F	F	R	I	T	A	H	C	L	A	Y	S	292	

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FIGURE 5D

hGALR3	N	S	C	L	N	P	L	V	Y	A	L	A	S	R	H	F	R	A	R	F	R	R	L	W	P	307
rGALR3	N	S	C	L	N	P	L	V	Y	S	L	A	S	R	H	F	R	A	R	F	R	R	L	W	P	307
rGALR1	N	S	S	V	N	P	I	I	Y	A	F	L	S	E	N	F	R	K	A	Y	K	Q	V	F	K	317
hGALR3	C	G	R	R	R	.	.	.	R	H	R	A	R	R	A	L	R	R	V	R	P	A	S	S	G	329
rGALR3	C	G	R	R	R	H	R	H	H	R	A	H	R	A	L	R	R	V	V	Q	P	A	S	S	G	332
rGALR1	C	R	V	C	N	E	S	P	H	G	D	A	K	E	K	N	R	I	D	T	P	P	S	T	N	342
hGALR3	P	P	G	C	P	G	D	A	R	P	S	G	R	L	L	A	G	G	G	Q	G	P	E	P	R	354
rGALR3	P	A	G	Y	P	G	D	A	R	P	R	G	W	S	M	E	P	R	350
rGALR1	C	T	H	V	346
hGALR3	E	G	P	V	H	G	G	E	A	A	R	G	P	E	368	
rGALR3	G	D	A	L	R	G	G	E	T	R	L	T	L	S	P	R	G	P	Q	370	

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FIGURE 6A

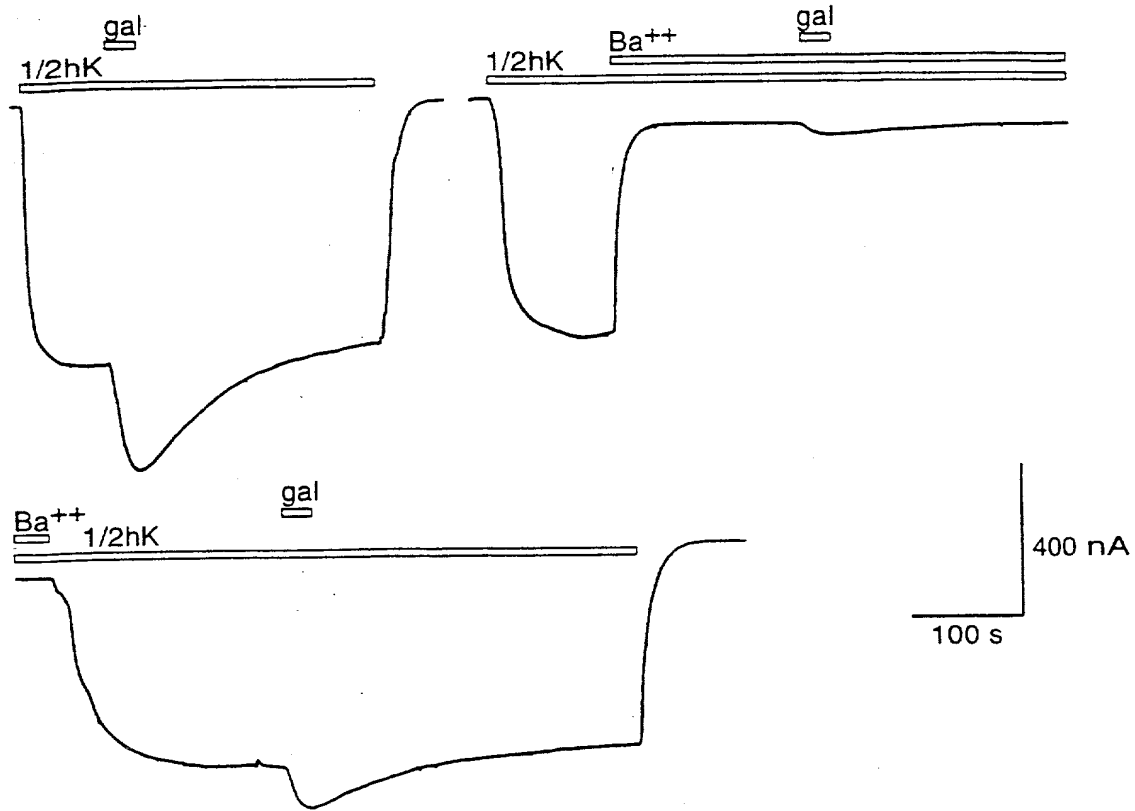
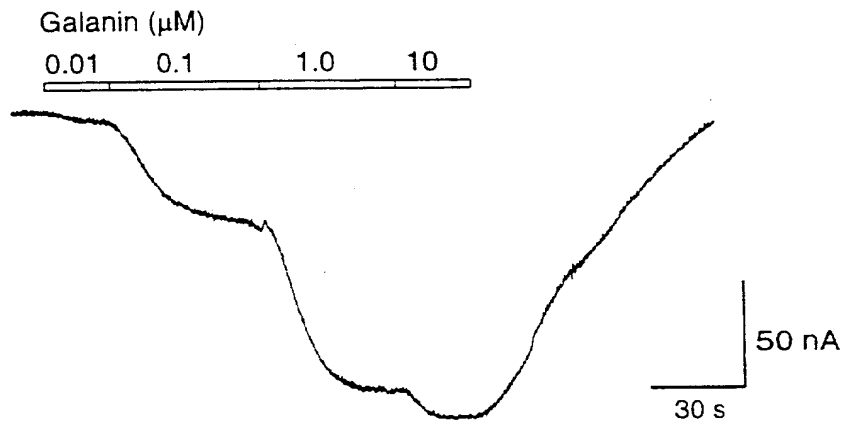


FIGURE 6B



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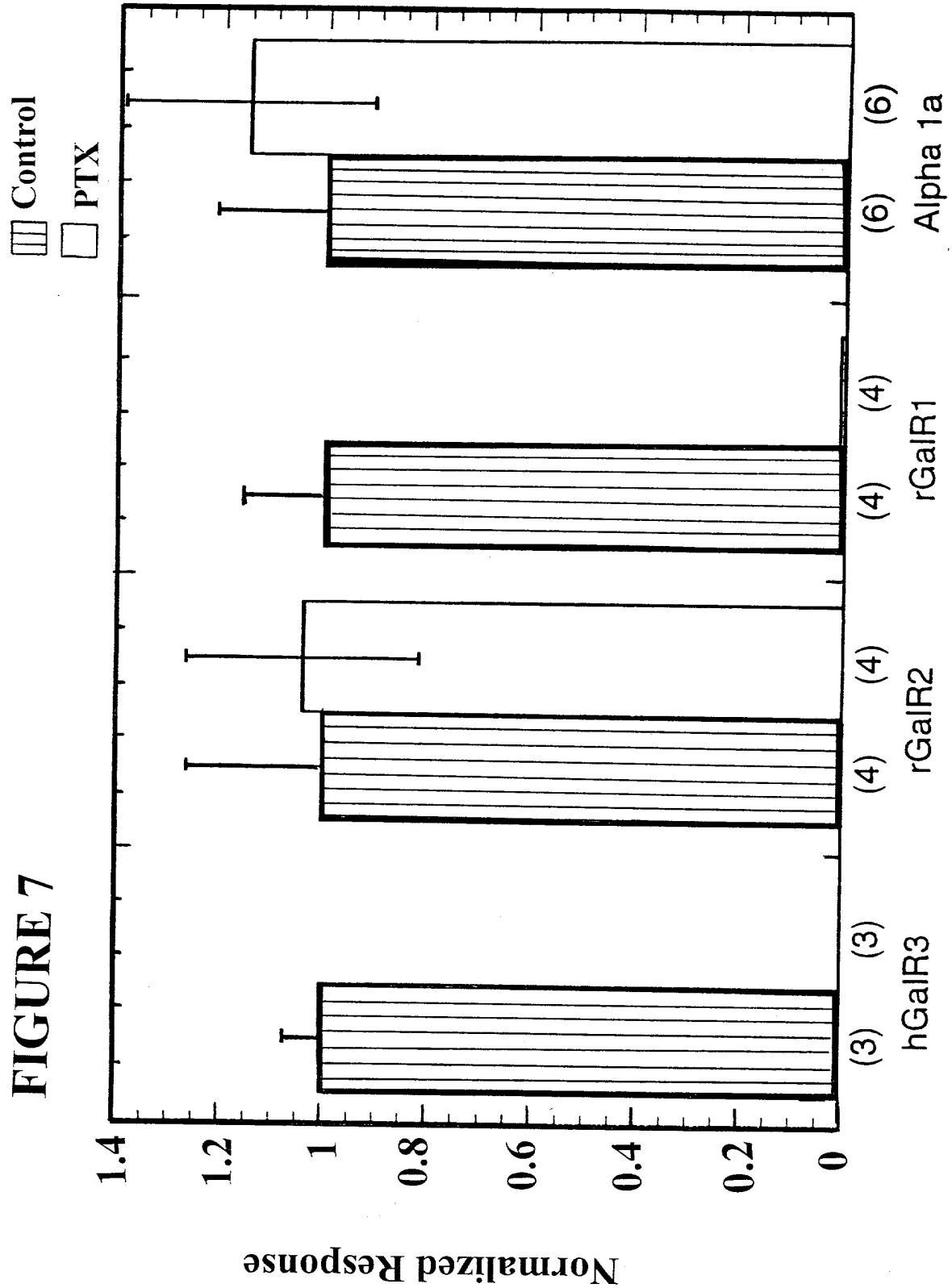


FIGURE 8A

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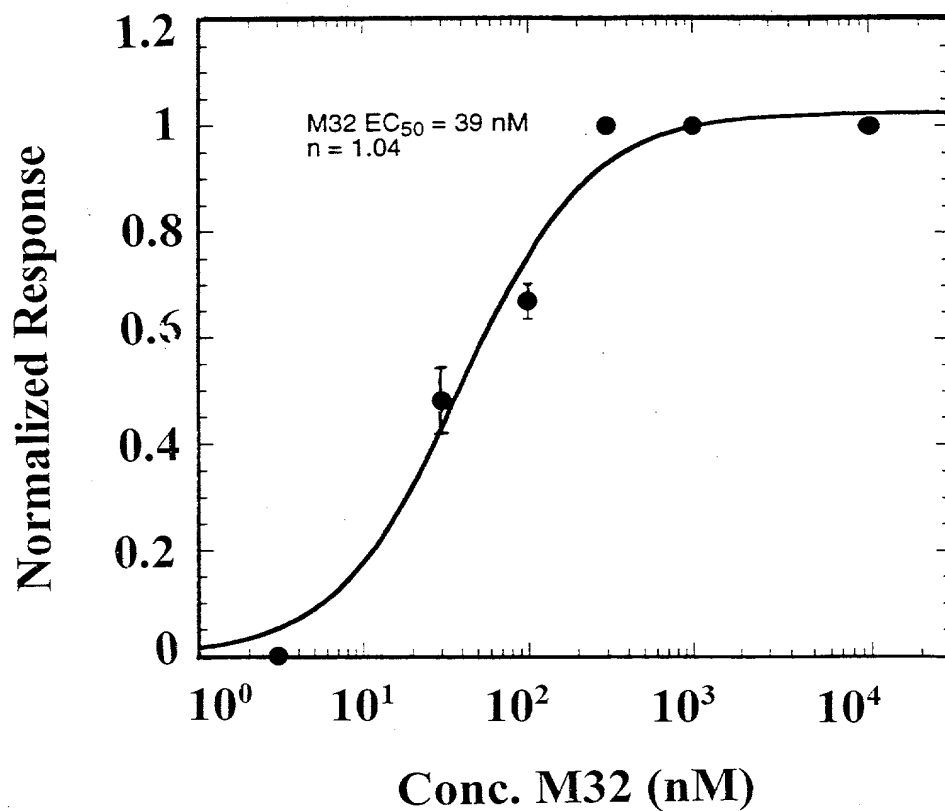


FIGURE 8B

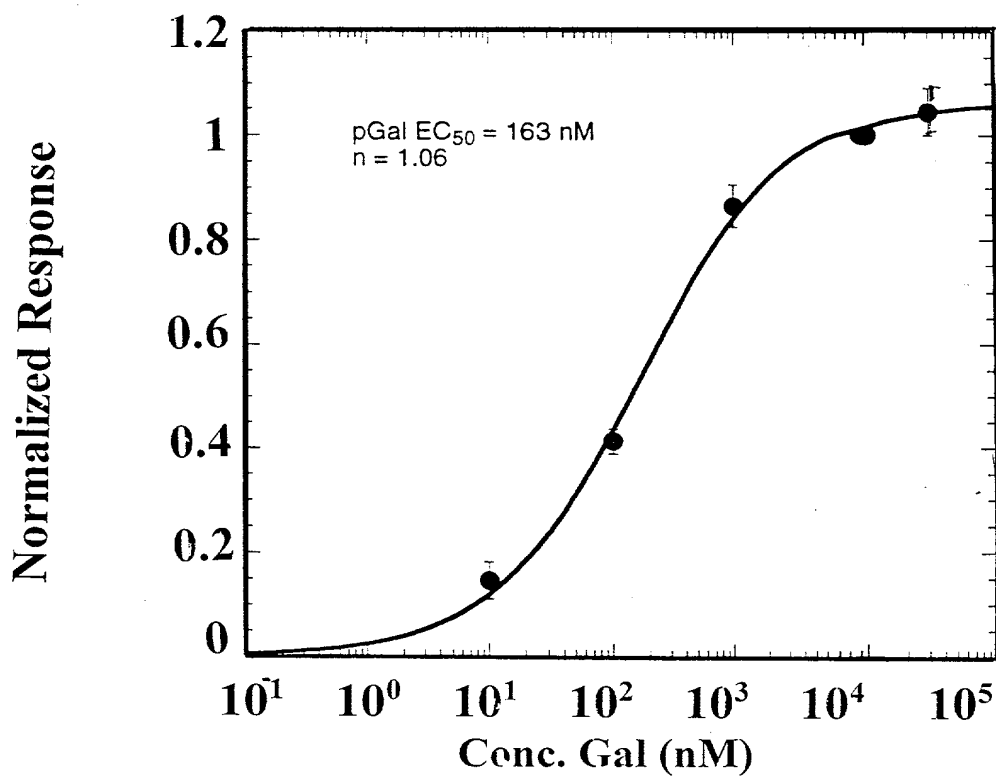


FIGURE 8C *12/19*

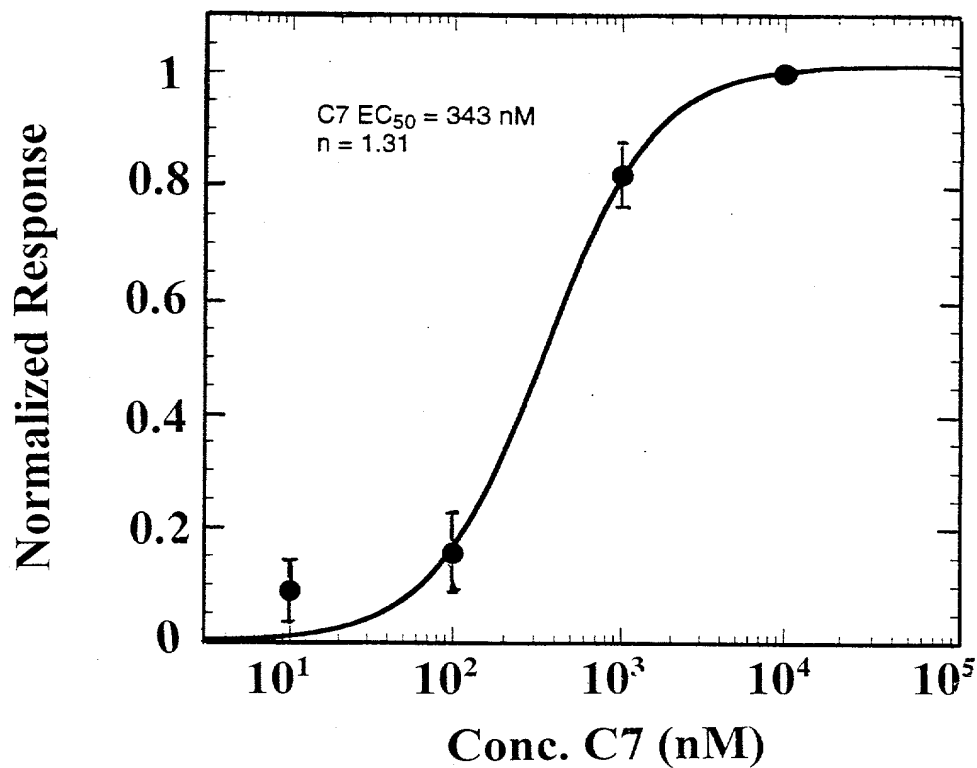


FIGURE 8D

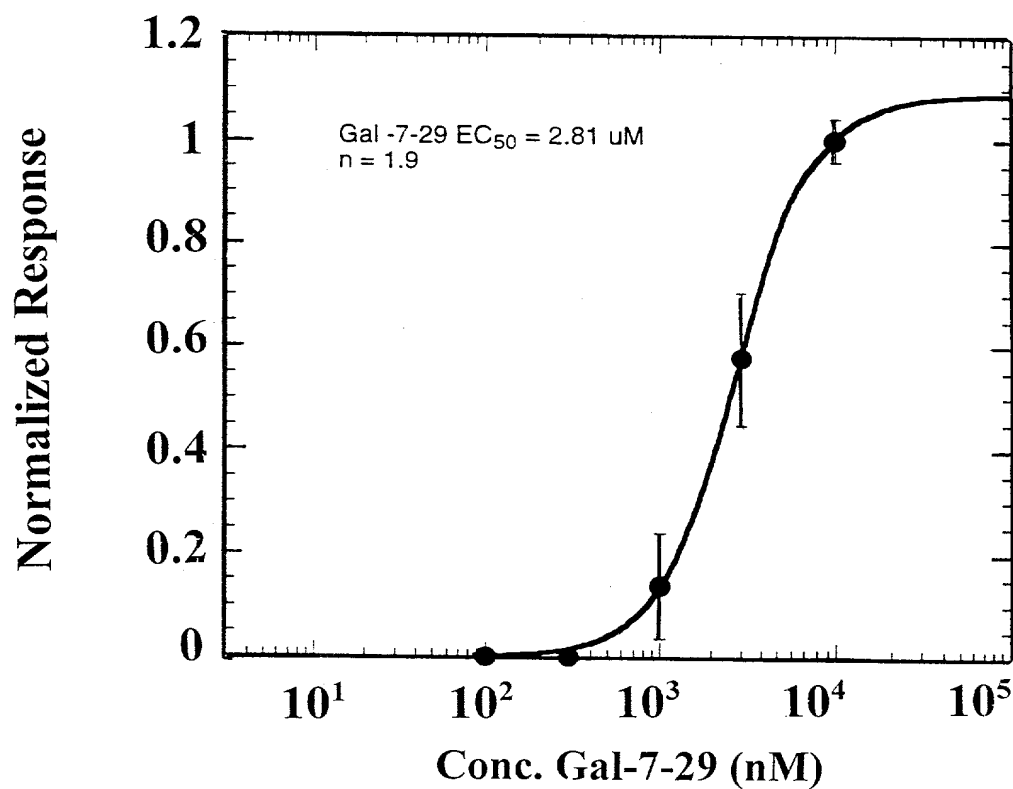


FIGURE 8E

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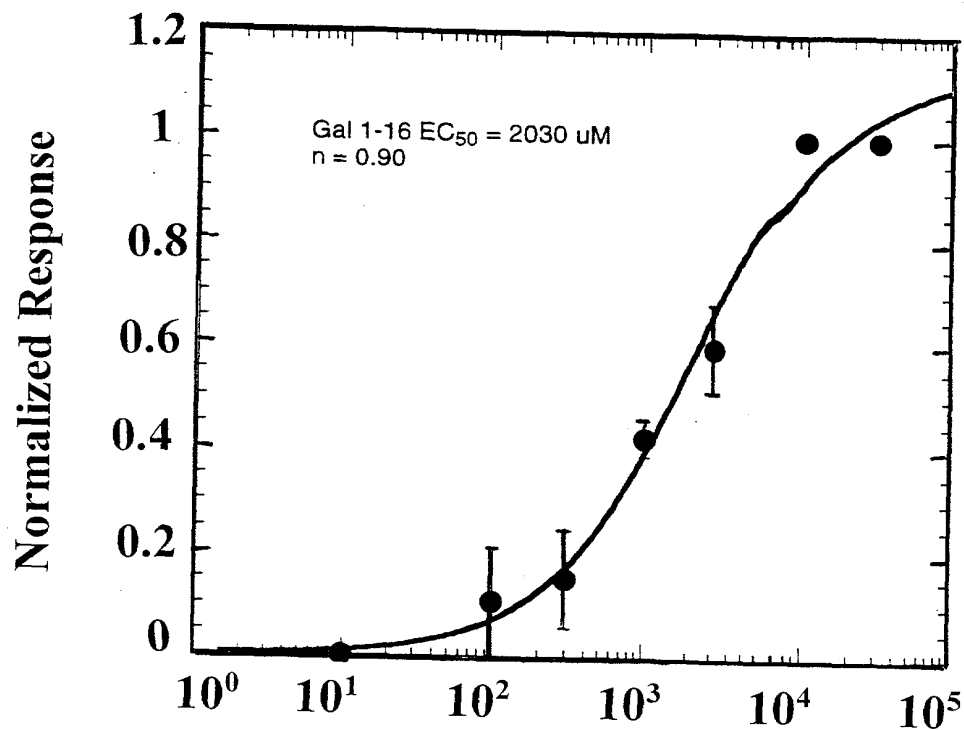
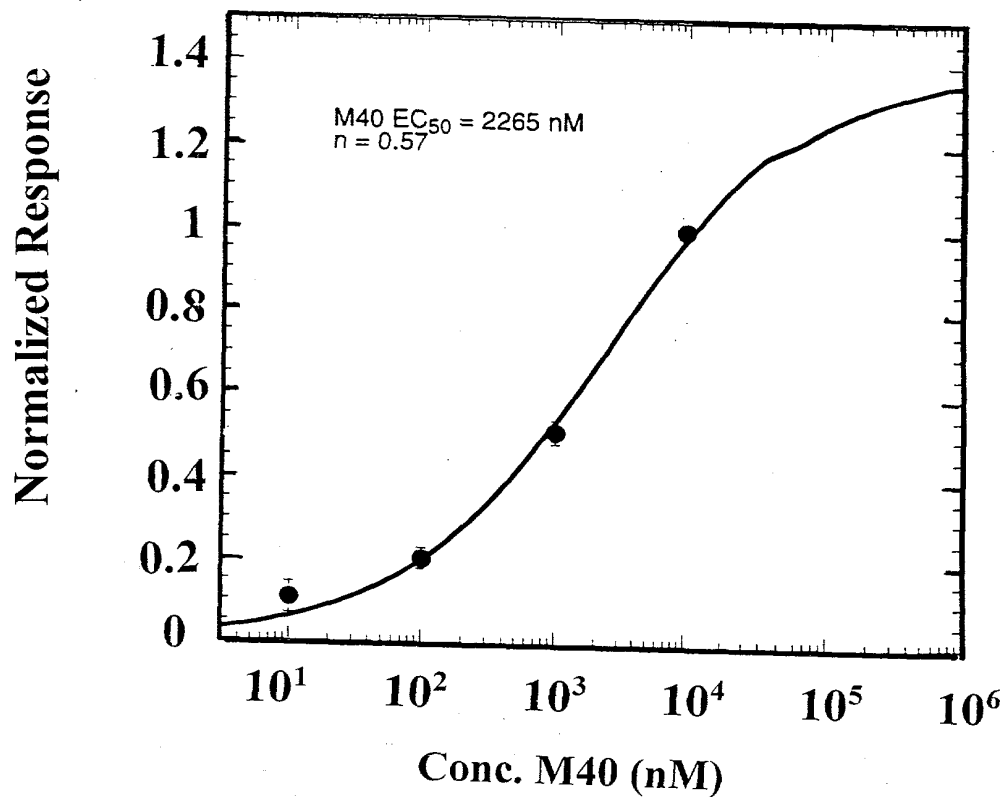


FIGURE 8F

Conc. Gal 1-16 (nM)



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FIGURE 9A

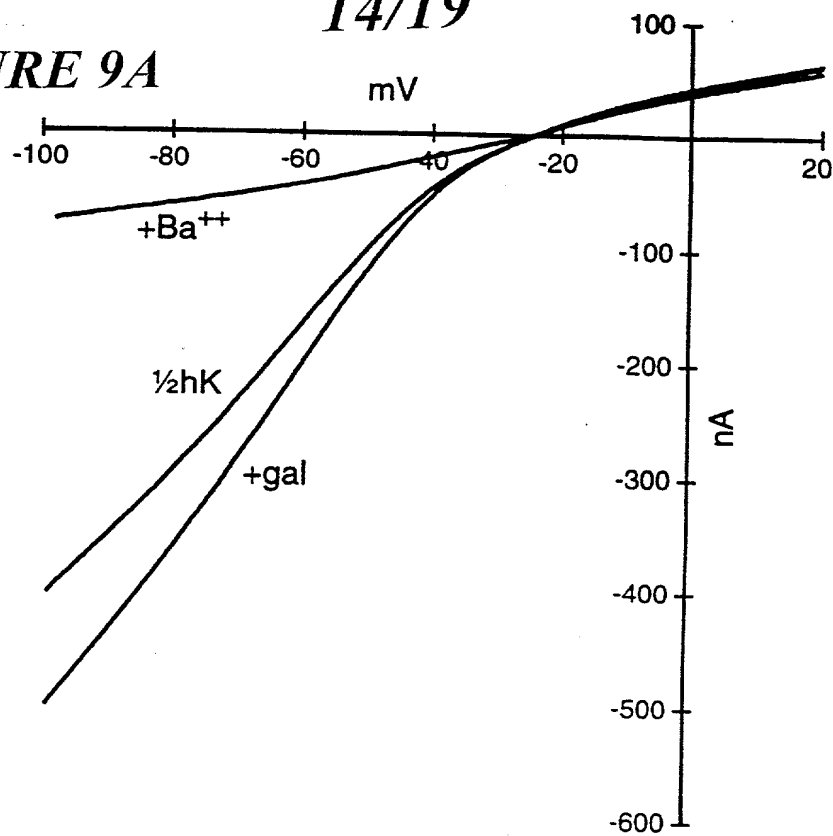
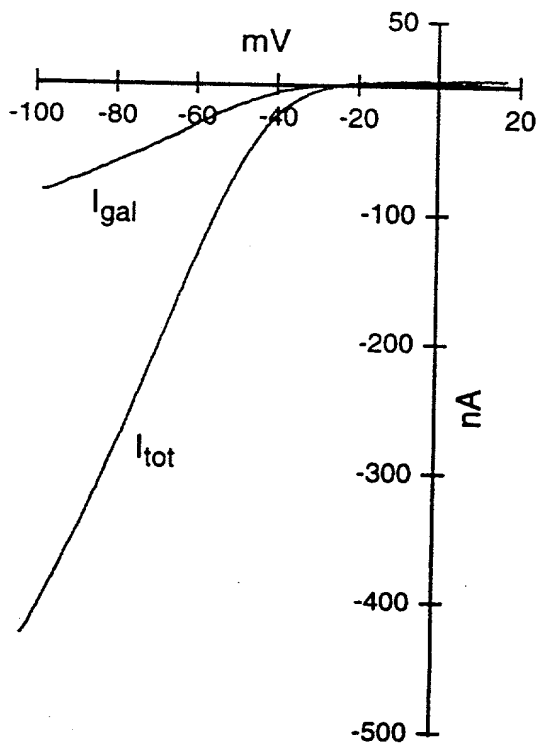


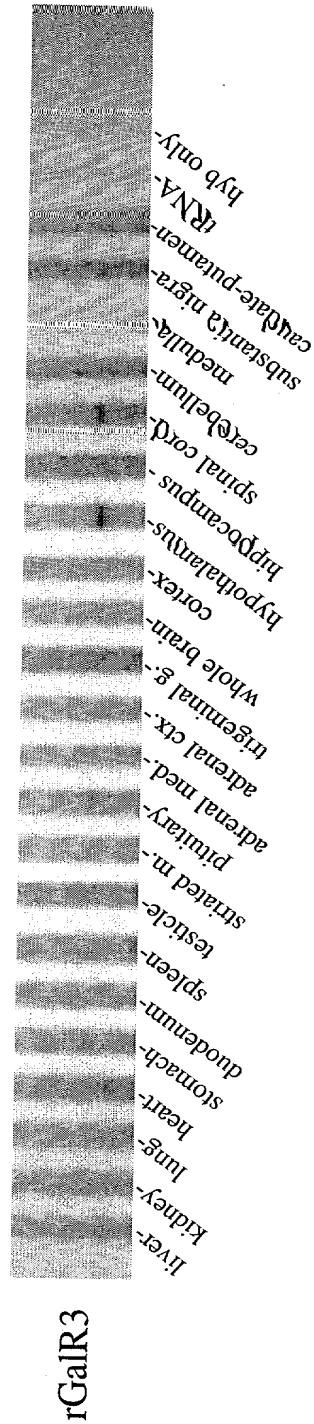
FIGURE 9B





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FIGURE 10

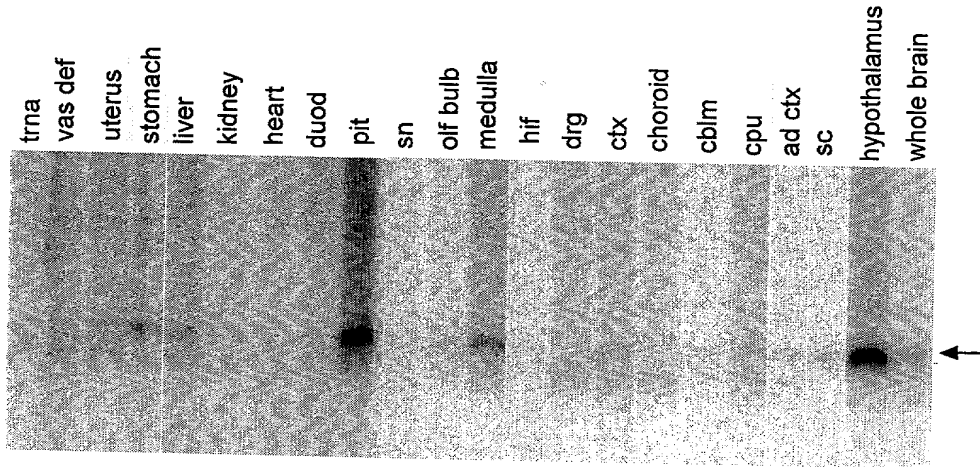


rGalR3

200140 1545000 F

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FIGURE 11



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FIGURE 12

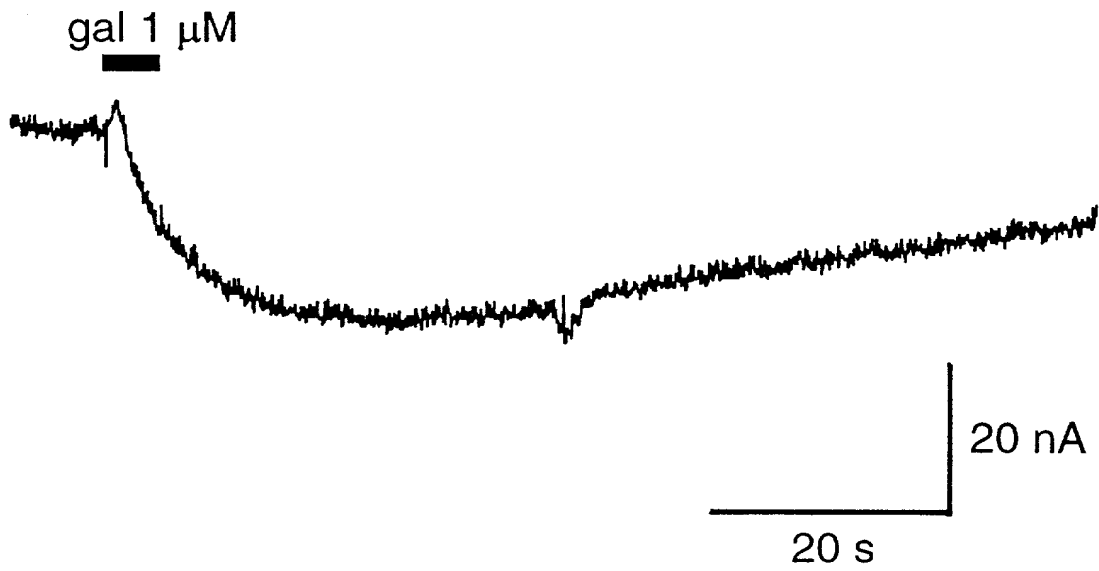
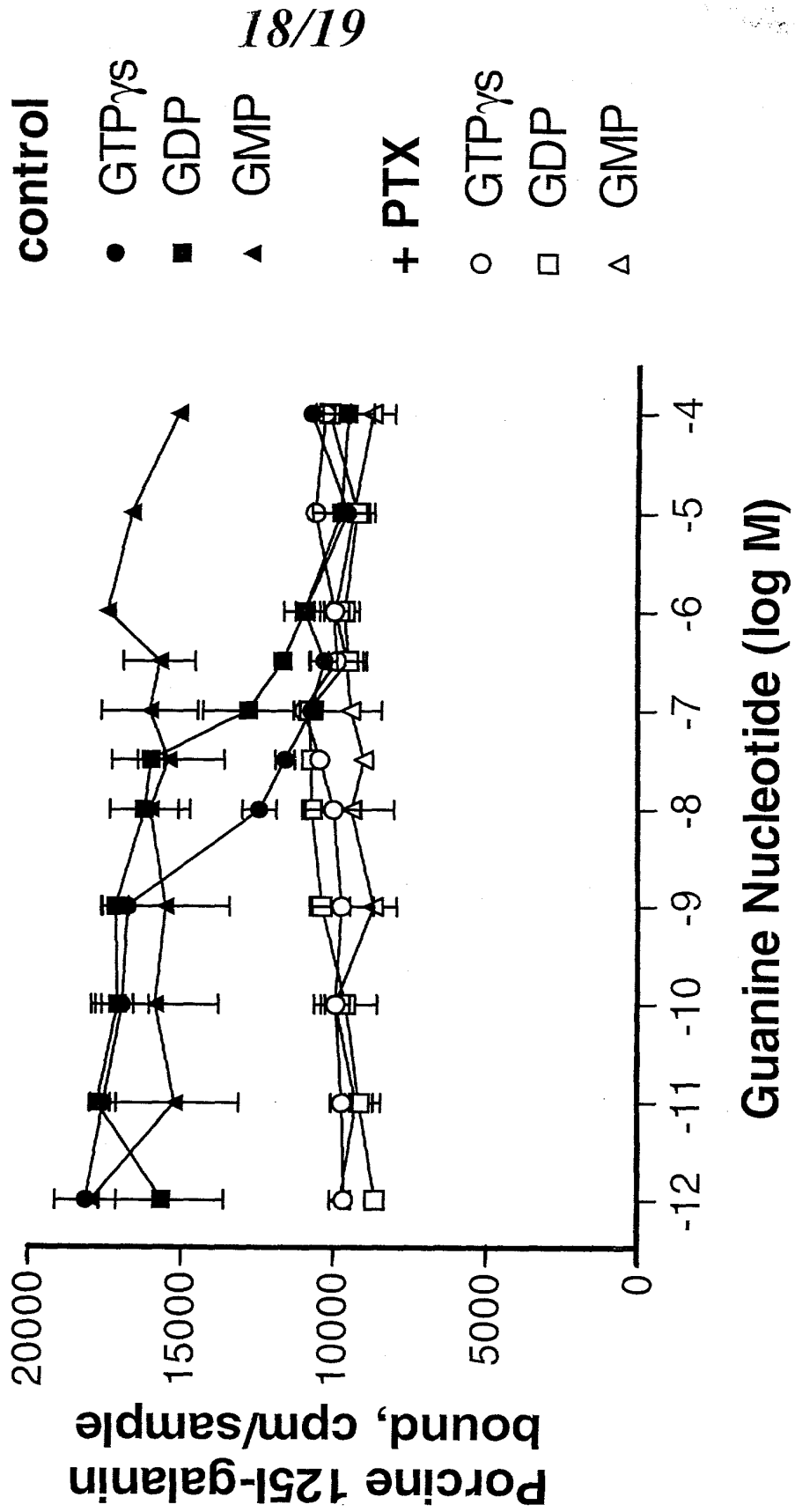


FIGURE 13A

hGALR3-LM #228
 +/- *Pertussis Toxin*

Guanine nucleotide effects



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FIGURE 13B

